IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of	)	
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Yoji SAKAGAMI et al.	)	Group Art Unit: Unassigned
	)	
Application No.: Unassigned	)	Examiner: Unassigned
	)	
Filed: June 14, 2000	)	
	)	
For: A PROMOTER DERIVED FROM PHYTOSULFOKINE PRECURSOR GENE	)	

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Prior to examination of the above-captioned patent application, kindly enter the following amendment.

IN THE SPECIFICATION:

Kindly replace the paragraph beginning at page 18, line 14 with the following:

The inventors searched the 5'-upstream region of the OsPSK gene for known motifs of other genes and found several potential regulatory elements (Fig. 4). The consensus sequence of a putative TATA box (5'-TATAA-3') was found at positions -63 to -68, referring to the transcription initiation site. Upstream to this sequence, there are one CAAT-box at -267 to -270 and three CCAAT-boxes at -906 to -910, -949 to -953, and -1074 to -1078, respectively. Interestingly, the sequence AACCCA (at -908) conforms to the A(A/C/G)CCCA consensus sequence, the binding site of a soybean enhancer for the

regulatory nuclear protein SEF3 (*Allen et al.*, 1989), and an 8-nucleotide enhancer core-like motif (*Weither et al.*, 1983; *Hata et al.*, 1986), located at position -1105 to -1112 with the sequence 5'-GTGGAAAG-3'. Additionally, three E-boxes (consensus sequence: 5'-CANNTG-3'; Pabo, 1992), three shear-stress-responsive elements (SSRE: 5'-GAGACC-3'; *Resnick et al.*, 1993), and several repetitive sequences are present in this 5'-end region. These findings suggest that transcription may be influenced by a variety of genetic elements.

IN THE CLAIMS:

Kindly replace claims 6-9, and add new claims 10-21 as follows.

6. (Amended) A plasmid in which the promoter according to claim 4 was incorporated.

7. (Amended) A transgenic plant cell in which the promoter according to claim 4 was incorporated to activate expression of a structural gene existing downstream of the promoter.

8. (Amended) A transgenic plant body in which the promoter according to claim 4 was incorporated to activate expression of a structural gene existing downstream of the promoter.

9. (Amended) A method to activate expression of an exogenous structural gene or an endogenous structural gene in a plant by incorporation of the promoter according to claim 4 into upstream of the structural gene.

10. (New) A plasmid in which the promoter according to claim 3 was incorporated.

11. (New) A plasmid in which the promoter according to claim 2 was incorporated.

12. (New) A plasmid in which the promoter according to claim 1 was incorporated.

13. (New) A transgenic plant cell in which the promoter according to claim 3 was incorporated to activate expression of a structural gene existing downstream of the promoter.

14. (New) A transgenic plant cell in which the promoter according to claim 2 was incorporated to activate expression of a structural gene existing downstream of the promoter.

15. (New) A transgenic plant cell in which the promoter according to claim 1 was incorporated to activate expression of a structural gene existing downstream of the promoter.

16. (New) A transgenic plant body in which the promoter according to claim 3 was incorporated to activate expression of a structural gene existing downstream of the promoter.

17. (New) A transgenic plant body in which the promoter according to claim 2 was incorporated to activate expression of a structural gene existing downstream of the promoter.

18. (New) A transgenic plant body in which the promoter according to claim 1 was incorporated to activate expression of a structural gene existing downstream of the promoter.

19. (New) A method to activate expression of an exogenous structural gene or an endogenous structural gene in a plant by incorporation of the promoter according to claim 3 into upstream of the structural gene.

20. (New) A method to activate expression of an exogenous structural gene or an endogenous structural gene in a plant by incorporation of the promoter according to claim 2 into upstream of the structural gene.

21. (New) A method to activate expression of an exogenous structural gene or an endogenous structural gene in a plant by incorporation of the promoter according to claim 1 into upstream of the structural gene.

REMARKS

By the present Preliminary Amendment, all multiple dependency has been eliminated from the original claims and new dependent claims 10-21 have been added so that the scope of the original multiple dependent claims has been preserved. It is to be understood that the revisions to the claims are solely for formalistic purposes and not with regard to patentability. Additionally, the specification has been amended to correct a typographical error.

Entry of the instant Preliminary Amendment and favorable consideration on the merits are respectfully requested.

Should the Examiner have any questions concerning the subject application, the Examiner is invited to contact the undersigned attorney at the number provided below.

Respectfully submitted,

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By: _____

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Date: June 14, 2001

Attachment to Preliminary Amendment dated June 14, 2001

Marked-up Copy

Page 18, Paragraph Beginning at Line 14

The [onventors] inventors searched the 5'-upstream region of the OsPSK gene for known motifs of other genes and found several potential regulatory elements (Fig. 4). The consensus sequence of a putative TATA box (5'-TATAA-3') was found at positions -63 to -68, referring to the transcription initiation site. Upstream to this sequence, there are one CAAT-box at -267 to -270 and three CCAAT-boxes at -906 to -910, -949 to -953, and -1074 to -1078, respectively. Interestingly, the sequence AACCCA (at -908) conforms to the A(A/C/G)CCCA consensus sequence, the binding site of a soybean enhancer for the regulatory nuclear protein SEF3 (*Allen et al.*, 1989), and an 8-nucleotide enhancer core-like motif (*Weither et al.*, 1983; *Hata et al.*, 1986), located at position -1105 to -1112 with the sequence 5'-GTGGAAAG-3'. Additionally, three E-boxes (consensus sequence: 5'-CANNTG-3'; Pabo, 1992), three shear-stress-responsive elements (SSRE: 5'-GAGACC-3'; *Resnick et al.*, 1993), and several repetitive sequences are present in this 5'-end region. These findings suggest that transcription may be influenced by a variety of genetic elements.

Attachment to Preliminary Amendment dated June 14, 2001

Marked-up Claims 6-9

6. (Amended) A plasmid in which the promoter according to [any one of claim 1 to] claim 4 was incorporated.

7. (Amended) A transgenic plant cell in which the promoter according to [any one of claim 1 to] claim 4 was incorporated to activate expression of a structural gene existing downstream of the promoter.

8. (Amended) A transgenic plant body in which the promoter according to [any one of claim 1 to] claim 4 was incorporated to activate expression of a structural gene existing downstream of the promoter.

9. (Amended) A method to activate expression of an exogenous structural gene or an endogenous structural gene in a plant by incorporation of the promoter according to [any one of claim 1 to] claim 4 into upstream of the structural gene.